

SEQUENCE LISTING

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Yamaguchi Kimura  
Shingo Sekine  
Kouju Kamata

<120> HUMAN GALECTIN-9-LIKE PROTEINS AND cDNAs ENCODING THESE PROTEINS

<130> GIN-6707CPUS

<140> 09/485,951  
<141> 2000-02-17

<150> 9-226468  
<151> 1997-08-22

<150> PCT/JP98/03670  
<151> 1998-08-19

<160> 11

<170> PatentIn Ver. 2.0

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<212> PRT  
<213> Homo sapiens

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35 40 45  
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

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Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly		
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Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val		
100	105	110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe		
115	120	125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr		
130	135	140
Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser		
145	150	155
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Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly		
165	170	175
Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile		
180	185	190
Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe		
195	200	205
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro		
210	215	220
Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser		
225	230	235
240		
Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile		
245	250	255
Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe		
260	265	270
Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly		
275	280	285
Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln		
290	295	300
Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala		
305	310	315
320		
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu		
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Val Gln Thr		

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ctg agt cca gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag 159  
Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Leu Gln  
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gcc ttc cac ttc aac cct cg 60 65 70  
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Ala Phe His Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys  
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aac acg agg cag aac gga agc tgg ggg ccc gag gag aag aca cac 351  
Asn Thr Arg Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His  
75 80 85 90  
atg cct ttc cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag 399  
Met Pro Phe Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln  
95 100 105  
agc tca gat ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac 447  
Ser Ser Asp Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr  
110 115 120  
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Phe His Arg Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly  
125 130 135  
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Ser Val Gln Leu Ser Tyr Ile Ser Phe Gln Asn Pro Arg Thr Val Pro  
140 145 150  
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Val Gln Pro Ala Phe Ser Thr Val Pro Phe Ser Gln Pro Val Cys Phe  
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Pro Pro Arg Pro Arg Gly Arg Arg Gln Lys Pro Pro Gly Val Trp Pro  
175 180 185  
gcc aac ccg gct ccc att acc cag aca gtc atc cac aca gtg cag agc 687  
Ala Asn Pro Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser  
190 195 200  
gcc cct gga cag atg ttc tct act ccc gcc atc cca cct atg atg tac 735  
Ala Pro Gly Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr  
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Pro His Pro Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly  
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Leu Tyr Pro Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser  
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Ala Gln Arg Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe  
255 260 265  
cac ctg aac ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag 927  
His Leu Asn Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln  
270 275 280  
atc gac aac tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg 975  
Ile Asp Asn Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met  
285 290 295  
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335 340 345  
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Asp Ile Gln Leu Thr His Val Gln Thr  
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Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn  
 35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro  
 50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly  
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Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly  
 85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val  
 100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe  
 115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr  
 130 135 140

Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser  
 145 150 155 160

Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly  
 165 170 175

Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile  
 180 185 190

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe  
 195 200 205

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro

210	215	220
Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser		
225	230	235
240		
Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile		
245	250	255
Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe		
260	265	270
Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly		
275	280	285
Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln		
290	295	300
Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala		
305	310	315
320		
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu		
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Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His		
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Val Gln Thr		
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Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn		
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Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro		
50	55	60
80		
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly		
65	70	75
80		
Ser Trp Gly Pro Glu Glu Arg Arg Thr His Met Pro Phe Gln Lys Met		
85	90	95
Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val Met		
100	105	110

Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe His  
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Arg Val Asp Thr Ile Phe Val Asn Gly Ser Val Gln Leu Ser Tyr Ile  
130 135 140

Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile Thr  
145 150 155 160

Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe Ser  
165 170 175

Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro Met  
180 185 190

Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser Ile  
195 200 205

Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile Asn  
210 215 220

Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Leu Arg Phe Asp  
225 230 235 240

Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly Ser  
245 250 255

Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln Ser  
260 265 270

Phe Ser Val Trp Ile Leu Cys Gly Ala His Cys Leu Lys Val Ala Val  
275 280 285

Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu Pro  
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Gln Thr

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Leu Gln Gly Thr Thr Lys Ser Phe Ala Gln Arg Phe Val Val Asn Phe  
35 40 45

Gln Asn Ser Phe Asn Gly Asn Asp Ile Ala Phe His Phe Asn Pro Arg  
50 55 60

Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly Ser  
65 70 75 80

Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly Met  
85 90 95

Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val Met  
100 105 110

Val Asn Gly Ile Leu Phe Val Gln Tyr Gln His Arg Val Pro Tyr His  
115 120 125

Leu Val Asp Thr Ile Ala Val Ser Gly Cys Leu Lys Leu Ser Phe Ile  
130 135 140

Thr Phe Gln Asn Ser Ala Ala Pro Val Gln His Val Phe Ser Thr Leu  
145 150 155 160

Gln Phe Ser Gln Pro Val Gln Phe Pro Arg Thr Pro Lys Gly Arg Lys  
165 170 175

Gln Lys Thr Gln Asn Phe Arg Pro Ala His Gln Ala Pro Met Ala Gln  
180 185 190

Thr Thr Ile His Met Val His Ser Thr Pro Gly Gln Met Phe Ser Thr  
195 200 205

Pro Gly Ile Pro Pro Val Val Tyr Pro Thr Pro Ala Tyr Thr Ile Pro  
210 215 220

Phe Tyr Thr Pro Ile Pro Asn Gly Leu Tyr Pro Ser Lys Ser Ile Met  
225 230 235 240

Ile Ser Gly Asn Val Leu Pro Asp Ala Thr Arg Phe His Ile Asn Leu  
245 250 255

Arg Cys Gly Gly Asp Ile Ala Phe His Leu Asn Pro Arg Phe Asn Glu  
260 265 270

Asn Ala Val Val Arg Asn Thr Gln Ile Asn Asn Ser Trp Gly Gln Glu  
275 280 285

Glu Arg Ser Leu Leu Gly Arg Met Pro Phe Ser Arg Gly Gln Ser Phe  
290 295 300

Ser Val Trp Ile Ile Cys Glu Gly His Cys Phe Lys Val Ala Val Asn  
305 310 315 320

Gly Gln His Met Cys Glu Tyr Tyr His Arg Leu Lys Asn Leu Gln Asp  
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Ile Asn Thr Leu Glu Val Ala Gly Asp Ile Gln Leu Thr His Val Gln  
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Thr

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<213> Artificial Sequence

<220>  
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